



SEQUENCE LISTING

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ROSCAM-SZPIRER, Josiane

<120> NON-HUMAN GENETICALLY MODIFIED MAMMAL LACKING THE ALPHA-FETOPROTEIN

<130> VANM243.1APC1

<140> US 10/031,021
<141> 2002-01-14

<150> PCT/BE00/00081
<151> 2000-07-11

<140> US 60/143,269
<141> 1999-07-12

<160> 8

<170> PatentIn version 3.1

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<212> DNA
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<223> N-Mer1 primer

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Met Lys Trp Ile Thr
1 5

ccc gct tcc ctc atc ctc ctg cta cat ttc gct gcg tcc aaa gca ttg 104
Pro Ala Ser Leu Ile Leu Leu Leu His Phe Ala Ala Ser Lys Ala Leu

gca aat ttt act gag att cag aag ctg gcc ctg gat gtg gct cac atc	824
Ala Asn Phe Thr Glu Ile Gln Lys Leu Ala Leu Asp Val Ala His Ile	
250 255 260	
cac gag gag tgt tgc caa gga aac tcg ctg gag tgt ctg cag gat ggg	872
His Glu Glu Cys Cys Gln Gly Asn Ser Leu Glu Cys Leu Gln Asp Gly	
265 270 275	
gaa aaa gtc atg aca tat ata tgt tct caa caa aat att ctg tca agc	920
Glu Lys Val Met Thr Tyr Ile Cys Ser Gln Gln Asn Ile Leu Ser Ser	
280 285 290	
aaa ata gca gag tgc tgc aaa tta ccc atg atc caa cta ggc ttc tgc	968
Lys Ile Ala Glu Cys Cys Lys Leu Pro Met Ile Gln Leu Gly Phe Cys	
295 300 305	
ata att cac gca gag aat ggc gtc aaa cct gaa ggc tta tct cta aat	1016
Ile Ile His Ala Glu Asn Gly Val Lys Pro Glu Gly Leu Ser Leu Asn	
310 315 320 325	
cca agc cag ttt ttg gga gac aga aat ttt gcc caa ttt tct tca gag	1064
Pro Ser Gln Phe Leu Gly Asp Arg Asn Phe Ala Gln Phe Ser Ser Glu	
330 335 340	
gaa aaa atc atg ttc atg gca agc ttt ctt cat gaa tac tca aga act	1112
Glu Lys Ile Met Phe Met Ala Ser Phe Leu His Glu Tyr Ser Arg Thr	
345 350 355	
cac ccc aac ctt cct gtc tca gtc att cta aga att gct aaa acg tac	1160
His Pro Asn Leu Pro Val Ser Val Ile Leu Arg Ile Ala Lys Thr Tyr	
360 365 370	
cag gaa ata ttg gag aag tgt tcc cag tct gga aat cta cct gga tgt	1208
Gln Glu Ile Leu Glu Lys Cys Ser Gln Ser Gly Asn Leu Pro Gly Cys	
375 380 385	
cag gac aat ctg gaa gaa gaa ttg cat aaa cac atc gag gag agc cag	1256
Gln Asp Asn Leu Glu Glu Glu Leu His Lys His Ile Glu Glu Ser Gln	
390 395 400 405	
gca ctg tcc aag caa agc tgc gct ctc tac cag acc tta gga gac tac	1304
Ala Leu Ser Lys Gln Ser Cys Ala Leu Tyr Gln Thr Leu Gly Asp Tyr	
410 415 420	
aaa tta caa aat ctg ttc ctt att ggt tac acg agg aaa gcc cct cag	1352
Lys Leu Gln Asn Leu Phe Leu Ile Gly Tyr Thr Arg Lys Ala Pro Gln	
425 430 435	
ctg acc tca gca gag ctg atc gac ctc acc ggg aag atg gtg agc att	1400
Leu Thr Ser Ala Glu Leu Ile Asp Leu Thr Gly Lys Met Val Ser Ile	
440 445 450	
gcc tcc acg tgc tgc cag ctc agc gag gag aaa tgg tcc ggc tgt ggt	1448
Ala Ser Thr Cys Cys Gln Leu Ser Glu Glu Lys Trp Ser Gly Cys Gly	
455 460 465	

gag gga atg gcc gac att ttc att gga cat ttg tgt ata agg aat gaa 1496
 Glu Gly Met Ala Asp Ile Phe Ile Gly His Leu Cys Ile Arg Asn Glu
 470 475 480 485

gca agc cct gtg aac tct ggt atc agc cac tgc tgc aac tct tcg tat 1544
 Ala Ser Pro Val Asn Ser Gly Ile Ser His Cys Cys Asn Ser Ser Tyr
 490 495 500

tcc aac agg agg cta tgc atc acc agt ttt ctg agg gat gaa acc tat 1592
 Ser Asn Arg Arg Leu Cys Ile Thr Ser Phe Leu Arg Asp Glu Thr Tyr
 505 510 515

gcc cct ccc cca ttc tct gag gat aaa ttc atc ttc cac aag gat ctg 1640
 Ala Pro Pro Pro Phe Ser Glu Asp Lys Phe Ile Phe His Lys Asp Leu
 520 525 530

tgc caa gct cag ggc aaa gcc cta cag acc atg aaa caa gag ctt ctc 1688
 Cys Gln Ala Gln Gly Lys Ala Leu Gln Thr Met Lys Gln Glu Leu Leu
 535 540 545

att aac ctg gtg aag caa aag cct gaa ctg aca gag gag cag ctg gcg 1736
 Ile Asn Leu Val Lys Gln Lys Pro Glu Leu Thr Glu Glu Gln Leu Ala
 550 555 560 565

gct gtc act gca gat ttc tcg ggc ctt ttg gag aag tgc tgc aaa gcc 1784
 Ala Val Thr Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Lys Ala
 570 575 580

cag gac cag gaa gtc tgt ttc aca gaa gag ggt cca aag ttg att tcc 1832
 Gln Asp Gln Glu Val Cys Phe Thr Glu Glu Gly Pro Lys Leu Ile Ser
 585 590 595

aaa act cgt gat gct ttg ggc gtt taaacatctc cagaaggaag agtggacaaa 1886
 Lys Thr Arg Asp Ala Leu Gly Val
 600 605

aaaatgtgtt gacgcttttg tgtgagcctt ttggcttaac tgtaactgct agtactttta 1946

ccacatggtg aagatgtcca tgtgagattt ctatacctta ggaataaaaa cttttcaact 2006

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<400> 8

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 20 25 30

Asp Ser Ser Gln Cys Val Thr Glu Lys Asn Val Leu Ser Ile Ala Thr

Ile	Thr	Phe	Thr	Gln	Phe	Val	Pro	Glu	Ala	Thr	Glu	Glu	Glu	Val	Asn
50						55					60				
Lys	Met	Thr	Ser	Asp	Val	Leu	Ala	Ala	Met	Lys	Lys	Asn	Ser	Gly	Asp
65					70					75					80
Gly	Cys	Leu	Glu	Ser	Gln	Leu	Ser	Val	Phe	Leu	Asp	Glu	Ile	Cys	His
				85					90					95	
Glu	Thr	Glu	Leu	Ser	Asn	Lys	Tyr	Gly	Leu	Ser	Gly	Cys	Cys	Ser	Gln
			100					105						110	
Ser	Gly	Val	Glu	Arg	His	Gln	Cys	Leu	Leu	Ala	Arg	Lys	Lys	Thr	Ala
		115					120					125			
Pro	Ala	Ser	Val	Pro	Pro	Phe	Gln	Phe	Pro	Glu	Pro	Ala	Glu	Ser	Cys
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Lys	Ala	His	Glu	Glu	Asn	Arg	Ala	Val	Phe	Met	Asn	Arg	Phe	Ile	Tyr
145					150					155					160
Glu	Val	Ser	Arg	Arg	Asn	Pro	Phe	Met	Tyr	Ala	Pro	Ala	Ile	Leu	Ser
				165					170					175	
Leu	Ala	Ala	Gln	Tyr	Asp	Lys	Val	Val	Leu	Ala	Cys	Cys	Lys	Ala	Asp
			180					185					190		
Asn	Lys	Glu	Glu	Cys	Phe	Gln	Thr	Lys	Arg	Ala	Ser	Ile	Ala	Lys	Glu
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Leu	Arg	Glu	Gly	Ser	Met	Leu	Asn	Glu	His	Val	Cys	Ser	Val	Ile	Arg
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Lys	Phe	Gly	Ser	Arg	Asn	Leu	Gln	Ala	Thr	Thr	Ile	Ile	Lys	Leu	Ser
225					230					235					240
Gln	Lys	Leu	Thr	Glu	Ala	Asn	Phe	Thr	Glu	Ile	Gln	Lys	Leu	Ala	Leu
				245					250					255	
Asp	Val	Ala	His	Ile	His	Glu	Glu	Cys	Cys	Gln	Gly	Asn	Ser	Leu	Glu
			260					265					270		
Cys	Leu	Gln	Asp	Gly	Glu	Lys	Val	Met	Thr	Tyr	Ile	Cys	Ser	Gln	Gln
		275					280					285			
Asn	Ile	Leu	Ser	Ser	Lys	Ile	Ala	Glu	Cys	Cys	Lys	Leu	Pro	Met	Ile
	290					295					300				
Gln	Leu	Gly	Phe	Cys	Ile	Ile	His	Ala	Glu	Asn	Gly	Val	Lys	Pro	Glu
305					310					315					320
Gly	Leu	Ser	Leu	Asn	Pro	Ser	Gln	Phe	Leu	Gly	Asp	Arg	Asn	Phe	Ala
				325					330					335	
Gln	Phe	Ser	Ser	Glu	Glu	Lys	Ile	Met	Phe	Met	Ala	Ser	Phe	Leu	His

